
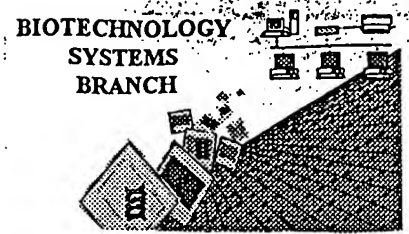


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## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/044,315  
Source: OIP  
Date Processed by STIC: 1/27/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

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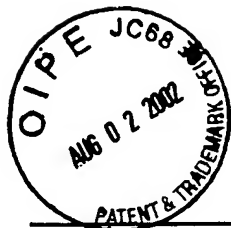
Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

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Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
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2011 South Clark Place, Arlington, VA 22202
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Revised 01/29/2002



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Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/044,315

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics  
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino  
Numbering The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0  
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences  
(OLD RULES) Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(ii) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences  
(NEW RULES) Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped-sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9 Use of n's or Xaa's  
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 Invalid <213>  
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) \_\_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0  
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



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OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/044,315

DATE: 01/27/2002  
TIME: 15:23:32

Input Set : A:\ES.txt  
Output Set: N:\CRF3\01272002\J044315.raw

Does Not Comply  
Corrected Diskette Needed

3 <110> APPLICANT: Boykin, David  
4 Tidwell, Richard  
5 Stringfellow, David  
6 Brock, Kenny  
7 Stephens, Chad  
8 Kumar, Arvind  
9 Wilson, W. David  
10 Givens, Daniel  
11 Dykstra, Christine  
13 <120> TITLE OF INVENTION: COMPOUNDS, METHODS AND COMPOSITIONS USEFUL FOR THE TREATMENT  
OF BOVINE  
14 VIRAL DIARRHEA VIRUS (BVDV) INFECTION AND HEPATITIS C VIRUS (HCV) INFECTION  
16 <130> FILE REFERENCE: 5470-333  
18 <140> CURRENT APPLICATION NUMBER: US/10/044,315  
18 <141> CURRENT FILING DATE: 2002-01-11  
18 <160> NUMBER OF SEQ ID NOS: 3  
20 <170> SOFTWARE: PatentIn version 3.1  
22 <210> SEQ ID NO: 1  
23 <211> LENGTH: 18  
24 <212> TYPE: DNA  
25 <213> ORGANISM: Primer *see item 10 on Erra Summary Sheet*  
27 <400> SEQUENCE: 1  
28 ggctagccat gcccttag 18  
31 <210> SEQ ID NO: 2  
32 <211> LENGTH: 17  
33 <212> TYPE: DNA  
34 <213> ORGANISM: Primer  
36 <400> SEQUENCE: 2 17  
37 ccatgtgcca tgtacag  
40 <210> SEQ ID NO: 3  
41 <211> LENGTH: 22  
42 <212> TYPE: DNA  
43 <213> ORGANISM: Primer  
45 <220> FEATURE:  
46 <221> NAME/KEY: D  
47 <222> LOCATION: (14)..(14)  
48 <223> OTHER INFORMATION: The novel BVD 180 primer was degenerate at the 14th base  
(D=G+A+T  
49 ) to accommodate differences within the 5' untranslated sequences  
50 of virus strains used in this research  
53 <400> SEQUENCE: 3  
54 cctgagtaca gggdagtcgt ca 22

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/044,315

DATE: 01/27/2002

TIME: 15:23:33

Input Set : A:\ES.txt

Output Set: N:\CRF3\01272002\J044315.raw

L:18 M:270 C: Current Application Number differs, Replaced Current Application No  
L:18 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:46 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3